

SEQUENCE LISTING

<110> Maliszewski, Charles R.
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<120> Inhibitors of Platelet Activation and Recruitment

<130> 2879-US

<140>
<141>

<150> US 60/104,585
<151> 1998-10-16

<150> US 60/107,466
<151> 1998-11-06

<150> US 60/149,010
<151> 1999-08-13

<150> PCT/US99/22955
<151> 1999-10-13

<160> 31

<170> PatentIn Ver. 2.0

<210> 1
<211> 1599
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (67)..(1596)

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ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108
Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val	65	70	75	300
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe	80	85	90	348
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu	95	100	105	110
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	115	120	125	396
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	130	135	140	444
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	145	150	155	492
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	160	165	170	540
ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	175	180	185	588
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	195	200	205	636
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act Glu Thr Phe Gly Ala Leu Asp Leu Gly Ala Ser Thr Gln Val Thr	210	215	220	684
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln	225	230	235	732
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu	240	245	250	780
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	255	260	265	828
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly	275	280	285	876
				924

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr 290 295 300	972
aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag cag ggt Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly 305 310 315	1020
att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn 320 325 330	1068
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu 335 340 345 350	1116
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val 355 360 365	1164
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val 370 375 380	1212
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys 385 390 395	1260
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe 400 405 410	1308
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr 415 420 425 430	1356
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser 435 440 445	1404
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile 450 455 460	1452
cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val 465 470 475	1500
ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile 480 485 490	1548
ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val 495 500 505 510	1596
tag	1599

<210> 2
<211> 510
<212> PRT
<213> Homo sapiens

<400> 2
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1 5 10 15
Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
20 25 30
Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45
Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60
Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80
Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95
Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110
Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125
Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140
Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160
Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
 275 280 285
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320
 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
 325 330 335
 Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
 340 345 350
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
 355 360 365
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
 370 375 380
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
 385 390 395 400
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
 405 410 415
 Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
 465 470 475 480
 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
 485 490 495
 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
 500 505 510

<210> 3
 <211> 476
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 3
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20															30
Ile	Phe	Leu	Ser	Ser	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys
35															45
Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile
50															60
Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln
65															80
Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln
85															95
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala
100															110
Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu
115															125
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu
130															140
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro
145															160
Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala
165															175
Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys
180															190
Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr
195															205
Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val
210															220
Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg
225															240
Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr
245															255
Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val
260															270
Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys
275															285
Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg
290															300
Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly
305															320

Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser
325														330	335
Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro
340														345	350
Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys
355														360	365
Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu
370														375	380
Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser
385														390	400
Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly
405														410	415
Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	
420														425	430
Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala
435														440	445
Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala
450														455	460
Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr				
465														470	475

<210> 4
 <211> 476
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<220>
 <221> VARIANT
 <222> (39)
 <223> Any amino acid, preferably Cys or Ser

<400> 4
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Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60

Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln
65				70						75				80	
Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln
				85					90				95		
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala
				100				105				110			
Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu
				115				120				125			
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu
				130			135			140					
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro
				145			150			155			160		
Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala
				165				170				175			
Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Phe	Ser	Gln	Lys	
				180				185				190			
Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr
				195			200				205				
Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val
				210			215			220					
Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg
				225			230			235			240		
Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr
				245				250				255			
Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val
				260				265			270				
Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys
				275			280			285					
Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg
				290			295			300					
Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly
				305					315			320			
Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser
				325				330				335			
Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro
				340				345			350				
Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys
				355				360			365				

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 5
<211> 1365

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>

<221> CDS

<222> (1)..(1362)

<400> 5

gca cct act tca agt tct aca aag aaa aca cag cta act agt tca acc 48
Ala Pro Thr Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144
Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240
Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg	85	90	95	288
tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg Ser Gln His Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met	100	105	110	336
cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat Arg Leu Leu Arg Met Glu Ser Glu Leu Ala Asp Arg Val Leu Asp	115	120	125	384
gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala	130	135	140	432
agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile	145	150	155	480
aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile	165	170	175	528
gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu	180	185	190	576
ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile	195	200	205	624
gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr	210	215	220	672
aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu	225	230	235	720
tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu	245	250	255	768
agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser	260	265	270	816
gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro	275	280	285	864
ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His	290	295	300	912

caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln 305 310 315 320	960
tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly 325 330 335	1008
gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser 340 345 350	1056
gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys 355 360 365	1104
gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu 370 375 380	1152
aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu 385 390 395 400	1200
ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His 405 410 415	1248
ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr 420 425 430	1296
atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr 435 440 445	1344
cct ctc tcc cac tcc acc taa Pro Leu Ser His Ser Thr 450	1365

<210> 6
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 6
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15
Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
 35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
 50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
 65 70 75 80

Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
 85 90 95

Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
 100 105 110

Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
 115 120 125

Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
 130 135 140

Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
 145 150 155 160

Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
 165 170 175

Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
 180 185 190

Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
 195 200 205

Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
 210 215 220

Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
 225 230 235 240

Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
 245 250 255

Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
 260 265 270

Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
 275 280 285

Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
 290 295 300

Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
 305 310 315 320

Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
 325 330 335

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
420 425 430

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
435 440 445

Pro Leu Ser His Ser Thr
450

<210> 7
<211> 1437
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>
<221> CDS
<222> (1)..(1434)

<400> 7
atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys
20 25 30

aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac 144
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 192
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 240
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
65 70 75 80

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe 85 90 95	288
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu 100 105 110	336
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val 115 120 125	384
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu 130 135 140	432
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn 145 150 155 160	480
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu 165 170 175	528
ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser 180 185 190	576
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln 195 200 205	624
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr 210 215 220	672
ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln 225 230 235 240	720
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu 245 250 255	768
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile 260 265 270	816
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly 275 280 285	864
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr 290 295 300	912

aag	aga	ttt	gag	atg	act	ctt	cca	ttc	cag	cag	ttt	gaa	atc	cag	ggt	960
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	
305															320	
310															315	
att	gga	aac	tat	caa	caa	tgc	cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	1008
Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	
325															335	
acc	agt	tac	tgc	cct	tac	tcc	cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	1056
Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	
340															350	
cca	cca	ctc	cag	ggg	gat	ttt	ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	1104
Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	
355															365	
atg	aag	ttt	tta	aac	ttg	aca	tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	1152
Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	
370															380	
act	gag	atg	atg	aaa	aag	ttc	tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	1200
Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Ile	Lys		
385															400	
aca	tct	tac	gct	gga	gta	aag	gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	1248
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	
															405	
															410	
															415	
tct	ggt	acc	tac	att	ctc	tcc	ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	1296
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	
															420	
															425	
															430	
gct	gat	tcc	tgg	gag	cac	atc	cat	ttc	att	ggc	aag	atc	cag	ggc	agc	1344
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	
															435	
															440	
															445	
gac	gcc	ggc	tgg	act	ttg	ggc	tac	atg	ctg	aac	ctg	acc	aac	atg	atc	1392
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	
															450	
															455	
															460	
cca	gct	gag	caa	cca	ttg	tcc	aca	cct	ctc	tcc	cac	tcc	acc	taa		1437
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr			
465															470	
															475	

<210> 8
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 8
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75 80

His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 85 90 95

Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 100 105 110

Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
 130 135 140

Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
 145 150 155 160

Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
 165 170 175

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 180 185 190

Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205

Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220

Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 245 250 255

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 260 265 270

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300

Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315 320

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr
420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 9
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser
20

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 11
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
35 40

<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 12
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15
Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
20 25

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 13
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15
Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

<210> 14
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctccac gagcccc 87

<210> 15
 <211> 87
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
 gatcggggct cgtgggagag aggtgtggac aatggttgct cagctggat catgttggtc 60
 aggttcagca tgtagccaa agtccag 87

<210> 16
 <211> 740
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (42)..(737)

<400> 16
 cggtaaccgct agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56
 Glu Pro Arg Ser Cys 1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
 10 15 20

gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 152
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 25 30 35

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gac gtg agc cac 200
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 40 45 50

<210> 17
<211> 232
<212> PRT
<213> *Homo sapiens*

<400> 17
Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
		20						25				30			
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
		35					40					45			
Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val
		50				55			60						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
		65			70			75			80				
Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
		85					90					95			
Asp	Trp	Leu	Asn	Gly	Lys	Asp	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala
		100				105					110				
Leu	Pro	Ala	Pro	Met	Gln	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
		115					120			125					
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr
		130				135					140				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Arg
		145			150				155			160			
His	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
		165					170				175				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
		180				185					190				
Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe
		195				200				205					
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
		210				215			220						
Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
		225			230										

<210> 18

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

ctttccatcc tgagcaac

18

<210> 19

<211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
aaaaaaactag tcagaacaaa gctttgccag aaaaacg

36

<210> 20
<211> 24
<212> PRT
<213> Mus sp.

<400> 20
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser
20

<210> 21
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
ctagttctgg agactacaaa gatgacgatg acaaaaccca gaacaa

46

<210> 22
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22
agctttgttc tgggttttgt catcgatc tttgtatct ccagaa

46

<210> 23
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
 ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
 tgtccacacc tctctcccac tccacctaa 89

<210> 24
 <211> 89
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 24
 ggcccttaggt ggagtgggag agaggtgtgg acaatggttg ctcagctggg atcatgttgg 60
 tcaggttcag catgtagccc aaagtccag 89

<210> 25
 <211> 1464
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1461)

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 25
 atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys
 20 25 30

aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144
 Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Lys
 35 40 45

acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
 50 55 60

gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240
 Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
 65 70 75 80

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg 85 90 95	288
gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile 100 105 110	336
ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro 115 120 125	384
agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly 130 135 140	432
atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg Met Arg Leu Leu Arg Met Glu Ser Glu Leu Ala Asp Arg Val Leu 145 150 155 160	480
gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly 165 170 175	528
gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act Ala Arg Ile Ile Thr Gly Gln Glu Gly Ala Tyr Gly Trp Ile Thr 180 185 190	576
atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser 195 200 205	624
ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp 210 215 220	672
ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr 225 230 235 240	720
atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp 245 250 255	768
tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala 260 265 270	816
ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile 275 280 285	864
ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val 290 295 300	912

agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt		960
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu		
305	310	315
320		
cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc		1008
Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys		
325	330	335
cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc		1056
His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser		
340	345	350
cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt		1104
Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe		
355	360	365
ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca		1152
Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr		
370	375	380
tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc		1200
Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe		
385	390	395
400		
tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag		1248
Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys		
405	410	415
gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc		1296
Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser		
420	425	430
ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc		1344
Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile		
435	440	445
450		
cat ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc		1392
His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly		
455	460	
tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc		1440
Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser		
465	470	475
480		
aca cct ctc tcc cac tcc acc taa		1464
Thr Pro Leu Ser His Ser Thr		
485		

<210> 26
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 26

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
35 40 45

Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
50 55 60

Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
65 70 75 80

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
85 90 95

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
100 105 110

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
115 120 125

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
130 135 140

Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
145 150 155 160

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
165 170 175

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
180 185 190

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
195 200 205

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
210 215 220

Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
225 230 235 240

Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
245 250 255

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
260 265 270

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
275 280 285

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
290 295 300

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
 305 310 315 320

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
 325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
 340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
 355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
 370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
 385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
 405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
 420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
 435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
 450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
 465 470 475 480

Thr Pro Leu Ser His Ser Thr
 485

<210> 27
<211> 464
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 27
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro
20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr
35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly
50 55 60

Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser
65				70					75					80	
Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys
				85				90					95		
Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	Glu	Thr		
	100				105				110						
Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu
	115				120				125						
Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu
	130				135				140						
Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln
145				150				155					160		
Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys
				165				170					175		
Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn
				180				185					190		
Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln
	195				200				205						
Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala
	210				215				220						
Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser
	225				230				235					240	
Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys
				245				250					255		
Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His
	260						265					270			
Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro
	275						280					285			
Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile
	290				295						300				
Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu
	305					310				315				320	
Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile
				325				330					335		
Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr
	340						345					350			
Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu
	355					360					365				

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu
 370 375 380
 Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr
 385 390 395 400
 Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His
 405 410 415
 Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln
 420 425 430
 Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn
 435 440 445
 Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 450 455 460

<210> 28

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
130 135 140

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
 145 150 155 160
 Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
 165 170 175
 Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg
 180 185 190
 Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly
 195 200 205
 Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln
 210 215 220
 Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
 225 230 235 240
 Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
 245 250 255
 Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
 260 265 270
 Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
 275 280 285
 Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
 290 295 300
 Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr
 305 310 315 320
 Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
 325 330 335
 Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
 340 345 350
 Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
 355 360 365
 Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
 370 375 380
 Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
 385 390 395 400
 Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr
 405 410 415
 Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
 420 425 430
 Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
 435 440 445

Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
450 455 460

Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470

<210> 29
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 29
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile
35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu
65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val
100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg
130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
 225 230 235 240
 Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
 245 250 255
 Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
 260 265 270
 Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
 275 280 285
 Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
 290 295 300
 Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln
 305 310 315 320
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
 325 330 335
 Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
 340 345 350
 Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
 355 360 365
 Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
 370 375 380
 Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
 385 390 395 400
 Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
 405 410 415
 Leu Ser Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
 420 425 430
 His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
 435 440 445
 Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
 450 455 460
 Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 30
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu
20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser
115 120 125

Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
130 135 140

Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
145 150 155 160

Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
165 170 175

Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
180 185 190

Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
195 200 205

Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
210 215 220

Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
225 230 235 240

Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
245 250 255

Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
260 265 270

Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys
275 280 285

Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
290 295 300

Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
 305 310 315 320

Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
 325 330 335

Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe
 340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
 355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
 370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
 385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe
 405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
 420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
 435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
 50 55